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1/2/102

What is claimed is:

- 1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the luxS gene, chosen from the group consisting of
- a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,
 - b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,
 - c) polynucleotide which is complementary to the polynucleotides of a) or b), and
 - d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c),

the polypeptide preferably having the activity of the histidine kinase LuxS.

- 20 2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA which is capable of replication in coryneform bacteria.
 - 3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.
- 25 4. A polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.
 - 5. A DNA as claimed in claim 2 which is capable of replication, comprising

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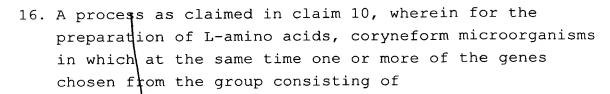
- the nucleotide sequence shown in SEQ ID No. 1,
- (ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or
- (iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii), and optionally
- (iv) sense mutations of neutral function in (i).
- 10 6. A DNA as claimed in claim 2 which is capable of replication, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.
 - 7. A polynucleotide sequence as claimed in claim 1, which codes for a polypeptide which comprises the amino acid sequences shown in SEQ ID No. 2.
 - 8. A coryneform bacterium in which the luxS gene is attenuated, in particular eliminated.
 - 9. The vector pCR2. luxSint, which
 - 9.1 carries an Internal fragment of the luxS gene 492 bp in size,
 - 9.2 the restriction map of which is reproduced in figure 1, and
 - 9.3 which is deposited in the E. coli strain
 Top10/pCR2.1luxSint under no. DSM 14082 at the
 Deutsche Sammlung für Mikroorganismen und
 Zellenkulturen [German Collection of
 Microorganisms and Cell Cultures].

- 10. A process for the fermentative preparation of L-amino acids, in particular lysine, which comprises carrying out the following steps:
- a) fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the luxS gene or nucleotide sequences which code for it are attenuated, in particular eliminated;
 - b) concentration of the L-amino acid in the medium or in the cells of the bacteria, and
- 10 c) isolation of the L-amino acid.
 - 11. A process as claimed in claim 10, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.
- 15 12. A process as claimed in claim 10, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.
- 13. A process as claimed in claim 10, wherein the
 20 expression of the polynucleotide(s) which code(s) for
 the luxS gene is attenuated, in particular eliminated.
 - 14. A process as claimed in claim 10, wherein the regulatory or catalytic properties of the polypeptide (enzyme protein) for which the polynucleotide luxS codes are reduced.
 - 15. A process as claimed in claim 10, wherein for the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of
- 30 15.1 the dapA gene which codes for dihydrodipicolinate synthase,

15.2

the gap gene which codes for glyceraldehyde 3-

phdsphate dehydrogenase, the tpi gene which codes for triose phosphate 15.3 isomerase, the pgk gene which codes for 3-phosphoglycerate 15.4 5 kinase, 15.5 the zwf gene which codes for glucose 6phosphate dehydrogenase, the pyc gene which codes for pyruvate 15.6 10 carboxylase, the mgo dene which codes for malate-quinone 15.7 oxidoreductase, the lysd gene which codes for a feed-back 15.8 resistant aspartate kinase, the lysE gene which codes for lysine export, 15.9 15 the hom gene which codes for homoserine 15.10 dehydrogena/se the ilvA gene which codes for threonine 15.11 dehydratase ϕ r the ilvA(Fbr) allele which codes for a feed back resistant threonine 20 dehydratase, the ilvBN gene which codes for acetohydroxy-15.12 acid synthase, the ilvD gene which codes for dihydroxy-acid 15.13 dehydratase, 25 the zwal gene which codes for the Zwal protein 15.14 is/are enhanced or over-expressed are fermented.



- 5 16.1 the pck gene which codes for phosphoenol pyruvate carboxykinase,
 - 16.2 the pgi gene which codes for glucose 6-phosphate isomerase,
 - 16.3 the poxB gene which codes for pyruvate oxidase
- 10 16.4 the zwa2 gene which codes for the Zwa2 protein is of are attenuated are fermented.
 - 17. A coryneform bacterium which contains a vector which carries parts of the polynucleotide but at least 15 successive nucleotides of the sequence as claimed in claim 1.
 - 18. A process as claimed in one or more of the preceding claims, wherein microorganisms of the species Corynebacterium glutamicum are employed.
- 19. A process for discovering RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which code for the histidine kinase LuxS or have a high similarity with the sequence of the luxS gene, which comprises employing the polynucleotide comprising the polynucleotide sequences as claimed in claims 1, 2, 3 or 4 as hybridization probes.